Application No: 10525449   Version No: 2.0

Input Set:

Output Set:

Started: 2010-08-19 09:01:23.662

Finished: 2010-08-19 09:01:26.090

Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 428 ms

Total Warnings: 10

Total Errors: 0

No. of SeqIDs Defined: 17

Actual SeqID Count: 17

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (1)
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
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W 213	Artificial or Unknown found in <213> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)

<110> POQUET, ISABELLE
      LLULL, DANIEL

<120> ZINC-REGULATED PROKARYOTIC EXPRESSION CASSETTES

<130> 40526U

<140> 10525449
<141> 2005-11-09

<150> PCT/FR03/02606
<151> 2003-08-29

<150> FR 02 10805
<151> 2002-08-30

<160> 17

<170> PatentIn version 3.5

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      sequence of the pzn bacterial promoter

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<220>
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Val Ser Ser Thr Ala Val Val Phe Ala
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gcgggctttt ttttgatatc gaattacccg ggaattcaga tctttgatca aggatctgtc   180

agctggttca actagcggtg gtcaaactgt tagtaataaa acttattgtt ttgatgttcg   240

gcttaaggat ggaaggattt ttcaaataaa aaagtaaaaa ataatgttaa ctggttgaca   300

ttattttttac tttgctatat aattaaccag taaactaatt atggaggaca aaatactatg   360

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atcttaatga ttctagctgc agaggtttcg acaaacgcga gaattgccga gcaactcaag        540

atttcgccag cagcggtaac taaagctctc aaaaaattac aagagcaaga actgattaaa        600

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ccagttgcta aagaacatgc tgctcatcat gagaaaactc taagtaccta ccaagaatta        720

ggagacaaat ttactgacga agaacaaaaa gtgataagtc aattcttatc agtacttacg        780

gaggagtttc gatgaagaaa atattgatgt tatttgctat tccggcagtt ttacttcttg        840

ctggttgtca aaaaacagca gacaaaccag aagttgtgac aactttttgag ccgatgtatg        900

aatttacgaa agcgattgtt ggagataagg ttaaaattga aaatattgtt ccggcgaatc        960

aagaagttca cgaatttgaa ccgagtgcca ttacgaaaaa aatggtagaa aatgcaaaga       1020

aaattgaagt cgagtttgac aaaggtcaaa gaactgataa atatggacgt ggcttagcgt       1080

atatttatgc tgatggaaaa                                                   1100


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gatgttcggc ttaaggatgg aaggattttt caaataaaaa agtaaaaaat aatgttaact        120

ggttgacatt atttttactt tgctatataa ttaaccagta                              160


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Val Ser Ser Thr Ala Val Val Phe Ala Tyr Ala
            20   25

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Phe Ala Glu Asn Lys His Glu Ile Leu Leu Gly Lys Cys Glu Ser Asp
            20   25   30

Val Lys Leu Thr Ser Thr Gln Glu His Ile Leu Met Leu Leu Ala Glu
        35   40   45

Gln Ile Ser Thr Asn Ala Lys Ile Ala Glu Lys Leu Lys Ile Ser Pro
    50   55   60

Ala Ala Val Thr Lys Ala Leu Lys Lys Leu Gln Glu Gln Glu Leu Ile
65   70   75   80

Lys Ser Ser Arg Ala Thr Asn Asp Glu Arg Val Val Leu Trp Ser Leu
            85   90   95

Thr Glu Lys Ala Val Pro Val Ala Lys Glu His Ala Thr His His Glu
            100   105   110

Lys Thr Leu Ser Thr Tyr Gln Glu Leu Gly Asn Lys Phe Thr Asp Glu
        115   120   125

Glu Gln Glu Val Ile Ser Lys Phe Leu Ser Ala Leu Thr Glu Glu Phe

Gln
145